

Figure 1

Sequence Name:

GW.S.ctg16335-000003.31.0

Figure 1A

LLAPTGSFLRNCTQDGWSETFPRPNLACGVNVNDSSNEKRSYLLKLKVMYTVGYSSSLVM
LLVALGILCAFRLRHCTRNYIHMHLFVSFILRALSNFIKDAVLFSSDDVTYCDAHRGCKL
VMVLFXYCIMANYSWLLVEGSTFTHxLAISFFSERKYLQGFVAFGWGSPAIFVALWAIAR
HFLEDVGCWDINANASIWWIIRGPVILSILNFIILRILMRKLRTQETRGNEVSHYK
RLARSTLLIPLFGIHYIVFAFSPEDAMEIQLFF

Figure 1B

CTCTTGGCACCCACAGGTTCTTGTCCGAAACTGCACACAGGATGGCTGGTCAGAAACC
TTCCCCAGGCATAATCTGGCCTGTGGCGTTAATGTGAACGACTCTCCAACGAGAACGG
CACTCCTACCTGCTGAAGCTGAAGTCATGTACACCGTGGGCTACAGCTCCTCCCTGGTC
ATGCTCCTGGTCGCCCTTGGCATCCTCTGTGCTTCCGGAGGCTCCACTGCACTCGCAAC
TACATCCACATGCACCTGTTCTGTCCTCATCCTCTGTGCCCTGTCCAACTTCATCAAG
GACGCCGTGCTCTTCTCCTCAGATGATGTACCTACTGCGATGCCACAGGGCGGGCTGC
AAGCTGGTCATGGTGTGTT

Figure 1C

TACTGCATCATGGCCAACACTACTCCTGGCTGCTGGTGGAAAGGCTCACCTCACACATNTC
CTCGCCATCTCCTTCTCTGAAAGAAAGTACCTCCAGGGATTGTGGCATTGGATGG
GGTTCTCCAGCCATTGGTGTGGCTATTGCCAGACACTTCTGGAAGATGTT
GGGTGCTGGGACATCAATGCCAACGCATCCATCTGGTGGATATTCTGGTGTGATC
CTCTCCATCCTGATTAATTCTACCTTTCATAAACATTCTAAGAATCCTGATGAGAAA
CTTAGAACCCAAGAAACAAGAGGAAATGAAGTCAGCATTATAAGGCCCTGCCAGGTCC
ACTCTCCTGCTGATCCCCCTTGGCATCCACTACATCGTCTCGCCTCTCCCCAGAG
GACGCTATGGAGATCCAGCTGTTTTT

Figure 1D

CTCTTGGCACCCACAGGTTCTTGTCCGAAACTGCACACAGGATGGCTGGTCAGAAACC
TTCCCCAGGCATAATCTGGCCTGTGGCGTTAATGTGAACGACTCTCCAACGAGAACGG
CACTCCTACCTGCTGAAGCTGAAGTCATGTACACCGTGGGCTACAGCTCCTCCCTGGTC
ATGCTCCTGGTCGCCCTTGGCATCCTCTGTGCTTCCGGAGGCTCCACTGCACTCGCAAC
TACATCCACATGCACCTGTTCTGTCCTCATCCTCTGTGCCCTGTCCAACTTCATCAAG
GACGCCGTGCTCTTCTCCTCAGATGATGTACCTACTGCGATGCCACAGGGCGGGCTGC
AAGCTGGTCATGGTGTGTT
TACTGCATCATGGCCAACACTACTCCTGGCTGCTGGTGGAAAGGCTCACCTCACACATNTC
CTCGCCATCTCCTTCTCTGAAAGAAAGTACCTCCAGGGATTGTGGCATTGGATGG
GGTTCTCCAGCCATTGGTGTGGCTATTGCCAGACACTTCTGGAAGATGTT
GGGTGCTGGGACATCAATGCCAACGCATCCATCTGGTGGATATTCTGGTGTGATC
CTCTCCATCCTGATTAATTCTACCTTTCATAAACATTCTAAGAATCCTGATGAGAAA
CTTAGAACCCAAGAAACAAGAGGAAATGAAGTCAGCATTATAAGGCCCTGCCAGGTCC
ACTCTCCTGCTGATCCCCCTTGGCATCCACTACATCGTCTCGCCTCTCCCCAGAG
GACGCTATGGAGATCCAGCTGTTTTT

Figure 2

Sequence Name:

GW.S.ctg16490-000000.17.0

Figure 2A

PTFILFSFQPGDKRTKHICVYWEGSEGGHWSTEGCSHVHSNGSYTKCKCFHLSSFAVLVA
LAPKDPVLTVITQVGLTISLLCLFLAILTFLLCRPIQNTSTSLLHLELSLCLFLAHLFLT
GINRTEPELCSIPIAGLLHFLYLAFCFTWMLLEGHLFLTVRNLKVANYTSTGRFKKRFMYP
VGYGIPAVIIAVSAIVGPQNYGTFTHCWLKLDKGFIWSFMGPVAVIILNLVFYFQVLWIL
RSKLSSLNKEVSTIQLDTRVMTFKAISQLFILGCSWGLGFFMVEEVGKTIGSIIAYSFTII
NTLQGVLLFVVHCLLNQRQR

Figure 2B

CCCACTTCTACTATTCTTTCCAGCCTGGTGACAAGAGAACAAAACATATCTGTGTC
TACTGGGAGGGATCAGAGGGAGGCCACTGGTCCACGGAGGGCTGCTCTCATGTGCACAGC
AACGGTTCTTACACCAAATGCAAGTGCTTCCATCTGTCAGCCTTGCCGTCCCTCGTGGCT
CTTGCCCCCAAGGAGGACCTGTGCTGACCGTGTACCCAGGTGGGCTGACCATCTCT
CTGCTGTGCCCTCTTCTGCCATCCACCTTCCCTGTGCCGCCATCCAGAACACC
AGCACCTCCCTCCATCTAGAGCTCTCCCTCTGCCCTCTCCTGGCCCACCTCCGTGTC
ACGGGCATCAACAGAACTGAGCCTGAGGTGCTGTGCTCCATATTGCAGGGCTGCTGCAC
TTCCTCTACCTGGCTTGCTTCACCTGGATGCTCTGGAAAGGGCTGCACCTCTCCTCACC
GTCAGGAACCTCAAGGTGGCCAATCACCCAGCACGGCAGATTCAAGAACAGGTTCATG
TACCCCTGTAGGCTACGGGATCCCAGCTGTGATTATTGCTGTGTCAGCAATAGTTGGACCC
CAGAATTATGGAACATTACTCACTGTTGGCTCAAGCTTGATAAAGGATTATCTGGAGC
TTCATGGGCCAGTAGCAGTCATTATCTTGATAAACCTGGTGTCTACTTCCAAGTTCTG
TGGATTTGAGAACAAACTTCTCCCTCAATAAGAACAGTTCCACCATTAGGACACC
AGAGTCATGACATTAAAGCCATTCTCAGCTATTATCCTGGGTGTTCTGGGCCTT
GGTTTTTATGGTTGAAGAACAGTAGGGAAAGACGATTGGATCAATATTGCATACTCATTC
ACCATCATCAACACCCTTCAGGGAGTGTGCTTTGTGGTACACTGTCTCCTTAATCGC
CAGGTAAGG

Figure 3

Sequence Name:

GW.S.ctg13100-000000.33.0

Figure 3A

QHSDAVHDLLDVITWVGILLSLVCLLICIFTFCFFRGLQSDRNTIHKNLCISLFVAELL
FLIGINRTDQPACAVFAALLHFFFLAAFTWMFLEGVQLYIMLVEVFESEHSRRKYFYLVG
YGMPALIVAVSAAVDYRSYGTDKVCWLRLDTYFIWSFIGPATLIIMNVIFLGIALYKMFH
HTAILKPESGCLDNIKLKINIPIKSIYIYMICMCV

Figure 3B

CAGCACAGTGATGCGGTCCATGACCTCCTCTGGATGTGATCACGTGGTTGGAATTTG
CTGTCCCTTGTGTTGTCTCCTGATTGCATCTCACATTGCTTTCCGGGGCTCCAG
AGTGACCGTAACACCATCCACAAGAACCTCTGCATCAGTCTTTGTAGCAGAGCTGCTC
TTCCTGATTGGGATCAACCGAACGTGACCAACCAATTGCCTGTGCTGTTTCCGCTGCCCTG
TTACATTTCTTCTTCTGGCTGCCTCACCTGGATGTTCTGGAGGGGGTGCAGCTTAT
ATCATGCTGGTGGAGGTTTGAGAGTGAAACATTACGTAGGAAATACTTTATCTGGTC
GGCTATGGATGCCTGCACTCATTGGCTGTGCAGCTGCAGTAGACTACAGGAGTTAT
GGAACAGATAAAGTATGGCTCCGACTTGACACCTACTTCATTGGAGTTTATAGGA
CCAGCAACTTGATAATTATGCTTAATGTAATCTCCTGGATTGCTTATATAAAATG
TTTCATCATACTGCTAACTGAAACCTGAATCAGGCTGTCTGATAACATCAAGTTAAA
ATTAATATTCCAATTATAAAATCTATTATATGTATATGATGTGTG

Figure 4

Sequence Name:

GW.A.ctg12444-000001.0.2

Figure 4A

GNVAVAFVYYKSIGPLLSSSDNFLLKPQNYDNSEEEERVISSVISVSMSSNPPTLYELEK
ITFTLSHRKTDYRSLCAFWNYPDTMNGWSSEGCELTYSNETHTSCRCNHLTHFAILM
SSGPSIIKDYNILTRITQLGIIISLICLAI CIFTFWFSEIQSTRTTIHKNLCCSLFLAE
LVFLVGINTNTNKFCIIAGLLHYFFLAFAWMCIEGIHLYLIVVGVIYNKGFLHKNFYI
FGYLSPAVVVGFSAAALGYRYYGTKVCWLSTENNFIWSFIGPACLIILVCIYKIVITI QK
SDDH

Figure 4B

GGCAATGTTGCAGTTGCATTGTATATTATAAGAGTATTGGTCCTTGCTTCATCATCT
GACAACCTCTTATTGAAACCTCAAAATTATGATAATTCTGAAGAGGAGGAAAGAGTCATA
TCTTCAGTAATTCAGTCTCAATGAGCTCAACACCACCCACATTATATGAACCTGAAAAA
ATAACATTTACATTAAGTCATCGAAAGGTACAGATAGGTATAGGAGTCTATGTGCATT
TGGAATTACTCACCTGATACCATGAATGGCAGCTGGCTTCAGAGGGCTGTGAGCTGACA
TACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCTGACACATTTGCAATTG
ATGTCCTCTGGTCCTTCATTGGTATTAAAGATTATAATATTCTACAAGGATCACTCAA
CTAGGAATAATTATTCACTGATTGTCTGCCATATGCATTTACCTCTGGTTCTTC
AGTGAATTCAAAGCACCAGGACAACAATTCACAAAAATCTTGCTGTAGCCTATTCTT
GCTGAACTGTTTCTTGTGGATCAATACAATAACTAATAAGCTCTGTCAATC
ATTGCCGGACTGCTACACTCTTTAGCTGCTTTGCATGGATGTGCATTGAAGGC
ATACATCTCATCTATTGGTGGGTGTCACTACAACAAGGGATTTGCAACAAGAAT
TTTATATCTTGCTATCTAACCCAGCCGTGGTAGTTGGATTTCGGCAGCACTAGGA
TACAGATATTATGGCACAACCAAAGTATGTGGCTAGCACCAGAAAACAACATTATTGG
AGTTTATAGGACCAGCATGCCTAATCATTCTGTATGTATATAAAATTGTTATTACA
ATTCAAAAAGTGTGATGATCAT

Figure 5

Sequence Name:

GW.S.ctg12789-000004.100.0

Figure 5A

GAWATTGCSVAALYLDSTACFCNHSTSFAILLQIYEVQGPPEESSLRTLSFGCGVSFCALTTTFLFLVAGVPKSERTTVHKNLTFSLASAEGFLMTSEWAKANEACVAVTVAMHFLFLVAWSWMLVEGLLLWRKVVAVSMHPGPGMRLYHATGWGVPGIVAVTLAMLPHDYVAPGHCWLNVHTNAIWAFVGVPVLFVLTWS

Figure 5B

GGTGCCTGGGCCACACAGGCTGCTCCGTTGGCTGCCCTGTACCTGGACTCCACCGCCTGCTTCTGCAACCACAGCACCAGCTTGCCTCCTGTCATAATCTATGAAGTACAGAGAGGGCCTGAGGAGGAGTCGCTGAGGACTCTGTCATTGTGGGCTGTGGCGTGTCCCTCTGCCCTCACCACCACTCTTGCCTCTTCTGGTGGCCGGGTCCCCAAGTCAGAGCGAACACAGTCCACAAGAACCTCACCTTCTCCCTGGCCTCTGCCGAGGGCTTCCCTCATGACCAGCGAGTGGCCAAGGCCATGAGGTGGCATGTGTGGCTGTACAGTCGCAATGCACTTCCCTTTCTGGTGGCATTCTCCTGGATGCTGGTGGAGGGGCTGCTGTGTGGAGGAAGGTGGTAGCTGTGAGCATGCACCCGGGCCAGGCATGCGGCTTACACGCCACAGGCTGGGGCGTGCCTGTGGCATCGTGGCGGTACCCCTGGCATGCTCCCCCATGACTACGTGGCCCCCGGACATTGCTGGCTCAATGTGCACACAAATGCCATCTGGGCCTTGTGGGGCTGTGCTCTCTGTGCTGACTGTGAGC

Figure 6

Sequence Name:

GW.A.ctg12776-000000.33.0

Figure 6A

MKSPPRTTLCLMFIVIYSSKAALNWNYESTIHPILLHEHEPAGEEALRQKRAVATKSPTAE
EYTVNIEISFENASFLDPIKAYLNSLSFPIHGNNTDQITDILSINVTTVCRPAGNEIWCS
CETGYGWPWERCLHNLCQERDVFLPGHCHSCLKEPPNGPFCLLQEDVTLNMRVRLNVG
FQEDLMNTSSALYRSYKTDLETARKGYGILPGFKGVTVTGFKSGSVVVTYEVKTPPSLE
LIHKANEQVQSLNQTYKMDYNSFQAVTINESNFFVTPEIIIFEGDTVSLVCEKEVLSSNV
SWRYEEQQLEIQNSSRFSIYTALFNNMTSVSKLTIHNIITPGDAGEYVCKLILDIFEYECK
KKIDVMPIQILANEEMKVMCDNNPVSLSNCCSQGNVNSKVEWKQEGKINIPGTETDIDS
SCSRYTLKADGTQCPSSGTTVITYCEFISAYGARGSANIKVTFISVANLTITPDPISV
SEQQNFSIKCISDVSNYDEVWNTSAGIKIYQRFYTRRYLDGAESVLTVKTSTREWNGT
YHCIFRYKNSYIATKDVIVHPLPLKNIMVDPLEATVSCSGSHIHKCCIEEDGDYKVTF
HTGSSSLPAAKEVNKKQVCYKHNFNASSVWSCKTVDVCCHTNAANNSVWSPSMKLNLV
PGENITCQDPVIGVGEPGKVIQKLCRFSNPSSPESPIGGTITYKCVGSQWEEKRNDCIS
APINSLLQMAKLIKSPSQDEMLPTYLKDLISIDKAEHIESSSPGSLGAIINILDLLSTV
PTQVNSEMMTBLSTVNVLGKPVNTWKVLQQWNTQSSQLLHSVERFSQALQSGDSPPL
SFSQTNVQMSMVIKSSHPETYQQRFVFPYFDLWGNVIDKSYLENLQSDSSIVTMAFP
LQAILAQDIQENNFAESLVMTTVSHNTMPFRISMFTKNNSPSGGETKCVFVNFRANN
TGGWDSSGCYVEEGDGDNVTCICDHLLTSFSILMSPDPSSLLGILLDIISYVGVGFSI
LSLAACLVVEAVVWKSVTKNRTSYMRHTCIVNIAASLLVANTWFIIVVAAIQDNRYILCKT
ACVAATFFIHFYLSVFFWMLTLGLMLFYRLVFILETSRSTQKAIACFCLGYGCPLAISV
ITLGATQPREVYTRKNVCWLNWEDTKALLAFAIPALIIVVVNITITIVVITKILRPSIGD
KPCQEKSSLFQISKSIGVLTPLGLTWGFLTTVFPGTNLVFHIIFAILNVQLFILLF
GCLWDLKQEALLNKFSLSRWSSQHSKTSLGSSPVFSMSSPISRRFNNLFGKTGTYNVST
PEATSSSLENSASSLLN

Figure 6B

ATGAAATCCCCAAGGAGAACCACTTGTGCCTCATGTTTATTGTGATTTATTCTTCAA
GCTGCACTGAACGGAAATTACGAGCTACTATTACATCCTTGAGTCTTCATGAACATGAA
CCAGCTGGTGAAGAGGCACTGAGGCCAAAACGAGCCGTTGCCACAAAAGTCCTACGGCT
GAAGAATAACACTGTTAATATTGAGATCAGTTGAAAATGCATCCTCCTGGATCCTATC
AAAGCCTACTTGAACAGCCTCAGTTCCAATTCATGGAATAACACTGACCAAATTACC
GACATTTGAGCATAAAATGTGACAACAGTCAGCAGACCTGCTGGAAATGAAATCTGGTGC
TCCTGCGAGACAGGGTATGGTGGCCTCGGAAAGGTGCTTCACAATCTCATTGTCAA
GAGCGTGACGTCTCCCTCCCAGGGCACCATTCAGCTGAGTGCCTAAAGAAACTGCCTCCAA
GGACCTTTGCCTGCTTCAGGAAGATGTTACCCCTGAACATGAGAGTCAGACTAAATGTA
GGCTTCAAGAAGACCTCATGAACACTTCCTCCGCCCTATAGGTCTACAAGACCGAC
TTGGAAACAGCGTCCGGAAGGGTACGGAATTTCACAGGCTCAAGGGGTGACTGTG
ACAGGGTTCAAGTCTGGAAGTGTGGTGTGACATATGAAGTCAGACTACACCACATCA
CTTGAGTTAACATAAAGCCAATGAACAAGTTGTCAGAGCCTCAATCAGACCTACAAA
ATGGACTACAACACTCCTTCAAGCAGTTACTATCAATGAAAGCAATTCTTGTACACCA
GAAATCATCTTGAAGGGGACACAGTCAGTCAGTGTGAAAGGAAGTTGTCTCC
AATGTGTCTGGCGCTATGAAGAACAGCAGTTGAAATCCAGAACAGCAGCAGATTCTCG
ATTTACACCGCACTTTCAACAAATGACTCGGTGTCCAAGCTCACCATCCACAACATC
ACTCCAGGTGATGCAGGTGAATATGTTGCAAACACTGATATTAGACATTTGAATATGAG
TGCAAGAAGAAAATAGATGTTATGCCCATCAAATTGGCAAATGAAGAAATGAAGGTG
ATGTGCGACAACAATCCTGTATCTTGAACCTGCTGCAGTCAGGGTAATGTTAATTGGAGC
AAAGTAGAATGGAAGCAGGAAGGAAAATAAATATTCCAGGAACCCCTGAGACAGACATA
GATTCTAGCTGCAGCAGATACACCTCAAGGCTGATGGAACCCAGTGCCCAAGCGGGTCA

TCTGGAACAACAGTCATCTACACTTGTGAGTCATCAGTGCCTATGGAGCCAGAGGAGT
GCAAACATAAAAGTGACATTCATCTCTGTGCCAATCTAACATAACCCCGACCCATT
TCTGTTCTGAGGGACAAAACCTTTCTATAAAATGCATCAGTGTGAGTAACATATGAT
GAGGTTTATTGGAACACTCTGCTGGAATTAAAATATACCAAGATTTATACCACGAGG
AGGTATCTTGATGGAGCAGAATCAGTACTGACAGTCAGACCTGACCAGGGAGTGGAT
GGAACCTATCACTGCATATTAGATATAAGAATTACATACAGTATTGCAACCAAAGACGTC
ATTGTTCACCCGCTGCCCTCAAAGCTAACATCATGGTGTGATCCTTGGAAAGCTACTGTT
TCATGCAGTGGTCCCACATCAAGTGCAGTAGAGGAGGATGGAGACTACAAAGTT
ACTTTCCATACGGGTCCTCATCCCTCCTGCTGCAAAGAAGTAACAAAAAACAGTG
TGCTACAAACACAATTCAATGCAAGCTCAGTTCTGGTGTCAAAAACGTTGATGTG
TGTTGTCACTTACCAATGCTGCTAATAATTCAAGTCTGGAGCCATCTATGAAGCTGAAT
CTGGTTCTGGGAAAACATCACATGCCAGGATCCGTAATAGGTGTCGGAGAGGCCGGG
AAAGTCATCCAGAAGCTATGCCGGTCTCAAACGTTCCAGCAGCCCTGAGAGTCCATT
GGCAGGACCATCACTTACAAATGTGAGGCTCCAGTGGCTAAGGCTTGATCAAGAGCCCCT
ATCTCTGCCCAATAAACAGTCTGCTCCAGATGGCTAAGGCTTGATCAAGAGCCCCT
CAGGATGAGATGCTCCCTACATACCTGAAGGATCTTCTATTAGCATAGACAAAGCGGAA
CATGAAATCAGCTCTCTGGGAGTCTGGGAGCCATTATTAACATCCTGATCTGCTC
TCAACAGTCCAACCCAAAGTAAATTCAAGAAATGATGACGCGACGTGCTCTACGGTTAAT
GTCATCCTGGCAAGCCCGTCTGAAACACCTGGAAGGTTTACAACAGCAATGGACCAAT
CAGAGTTCACAGCTACTACATTCAAGTGGAAAGATTCCCAAGCATTACAGTCGGGAGAT
AGCCCTCCTTGTCTCTCCAAACTAATGTGAGATGAGCAGATGGTAATCAAGTCC
AGCCACCCAGAAACCTATCAACAGAGGTTGTTCCCATCTTGACCTCTGGGCAAT
GTGGTCATTGACAAGAGCTATCTAGAAAACCTGAGTCGGATTGCTTGTACCATG
GCTTCCCAACTCTCCAAGCCATCCTGCCAGGATATCCAGGAAAATAACTTGCAGAG
AGCTTAGTGTGACAACCAACTGTGAGCCACAATACAACATGCCATTGAGGATTCAATG
ACTTTAAGAACAAATAGCCCTCAGGCGGCAAACGAAGTGTGCTCTGGAAACTCAGG
CTTGCCAACAAACACAGGGGGTGGGACAGCAGTGGGTGCTATGTAGAAGAAGGTGATGG
GACAATGTCACCTGTATCTGTGACCACCTAACATCATCTCCATCCTCATGCCCCGT
TCCCCAGATCCTAGTTCTCTGGAAATACTCCTGGATATTATTTCTATGTTGGGTG
GGCTTTCCATCTGAGCTGGCAGCCTGCTAGTTGTTGGAAGCTGTGGTGTGAAATCG
GTGACCAAGAACCGGACTTCTTATATGCGCCACACCTGCATAGTAATATGCTGCC
CTTCTGGTCGCCAACACCTGGTCATTGTGGTCGCTGCCATCCAGGACAATCGCTACATA
CTCTGCAAGACAGCCTGTCGGCTGCCACCTTCTCATCCACTTCTTACCTCAGCGTC
TTCTCTGGATGCTGACACTGGGCTCATGCTGTTCTATGCCCTGGTTTCATTCTGCAT
GAAACAAGCAGGTCCACTCAGAAAGCCATTGCCCTCTGCTTGTGCTATGGCTGCC
GCCATCTCGGTCACTCAGCTGGAGCCACCCAGCCCCGGAAAGTCTATACGAGGAAGAAT
GTCTGTTGGCTCAACTGGGAGGACACCAAGCCCTGCTGGCTTCGCCATCCCAGCACTG
ATCATTGTTGGTGGTGAACATAACCATCACTATTGTGGTCACTACCAAGATCTGAGG
TCCATTGGAGACAAGCCATGCAAGCAGGAGAAGAGCAGCCTGTTCACTGAGCAAGAGC
ATTGGGGTCTCACACCAACTCTGGGCTCACTTGGGTTTGGTCTCACCACGTGTT
CCAGGGACCAACCTTGTGTTCCATATCATATTGCCATCCTCAATGTCTCAGGGATTA
TTCATTTTACTCTTGGATGCCCTGGGACTGAGGTACAGGAAGCTTGCTGAATAAG
TTTCATTGTCGAGATGGCTTCAAGCAACTCAAGTCAACATCCCTGGGTCATCCACA
CCTGTGTTCTATGAGTTCTCAATATCAAGGAGATTAACAATTGTTGGTAAAACA
GGAACGTATAATGTTCCACCCAGAAGCAACCAGCTCATCCCTGGAAAACATCCAGT
GCTTCTCGTTGCTCAAC

Figure 7

Sequence Name:

GW.S.ctg12776-000000.175.0

Figure 7A

ILNSKSISNWTIFDRNSSYILLHSVNSFARRLFIDNIPVDISDVFIHTMGTISGDNIG
KNFTFSMRINDTSNEVTGRVLISRDELRKVPSQSQVISIAFPTIGAILEASLLENVTVNG
LVLSAILPKELKRISLIFEKISKSEERRTQCVGWHSVENRWDQQACKMIQENSQQAVCKC
RPSKLFTSFSILMSPHILESLILTYITYVGLGISICSLILCLSIEVLVWSQVTKTEITYL
RHVCIVNIAATLLMADWFIVASFLSGPITHHKGCVAATFFVHFFYLSVFFWMLAKALLI
LYGIMIVFHTLPKSVLVASLFSVGYGCPLAIAAITVAATEPGKGYLREICWLNWDMTKA
LLAFVIPALAIVVVNLTIVTIVKTQRAAIGNSMFQEVRRAIVRISKNIAILTPLGLTW
GFGVATVIDDRSLAFHIIFSLLNAFQFFILVFGTILDPKV

Figure 7B

ATTCTTAACAGCAAAAGCATCTCAACTGGACTTTCATTCTGACAGAAACAGCAGCTAT
ATCCTGCTACATTCACTCAGTCAACTCCTTGCAAGAAGGCATTCTCATAGATAACATCCCTGTT
GACATATCAGATGTCTTCAATTCAACTATGGCACCACCATATCTGGAGATAACATTGGA
AAAAATTCACTTTCTATGAGAATTAAATGACACCAGCAATGAAGTCAGTGGAGAGTG
TTGATCAGCAGAGATGAACCTCGGAAGGTGCCTCCCTCTCAGGTCACTCAGCATTGCA
TTTCCAACATTGGGCTATTTGGAAGCCAGTCTTGAAAATGTTACTGTAAATGGG
CTTGTCCCTGCTGCCATTGGCCAAGGAACCTAAAAGAATCTCACTGATTTGAAAAG
ATCAGCAAGTCAGAGGAGAGGAGGACACAGTGTGTTGGCTGGCACTCTGTGAGAACAGA
TGGGACCAGCAGGCCTGAAAATGATTCAAGAAAACCTCCAGCAAGCTGTTGCAAATGT
AGGCCAAGCAAATTGTTACCTCTTCAATTCTTACACATCTTACAGT
CTGATTCTGACTTACATCACATATGTAGGCCTGGCATTCTATTGCAAGCCTGATCCTT
TGCTTGTCCATTGAGGTCTAGTCTGGAGCCAAGTGACAAAGACAGAGATCACCTATT
GCCATGTGCATTGTTAACATTGCAGCCACTTGTGATGGCAGATGTGTTGCAATT
GTGGCTTCTTCTTACTGGCCAATAACACACCAAGGGATGTGTTGCAAGCATT
TTTGTTCATTCTTTACCTTCTGTATTTCTGGATGCTGCAAGGCACCTCTTATC
CTCTATGGAATCATGATTGTTCCATACCTTGGCCAAGTCAGTCTGGCTGGCATCTG
TTTCAGTGGCTATGGATGCCATTGGCATTGCTGCCATCACTGTTGCTGCCACTGAA
CCTGGCAAAGGCTATCTACGACCTGAGATCTGCTGGCTCAACTGGGACATGACCAAGCC
CTCCTGGCCTCGTGATCCCAGCTTGGCCATCGTGGTAGTAAACCTGATCACAGTCACA
CTGGTGATTGTCAAGACCCAGCGAGCTGCCATTGGCAATTCCATGTTCCAGGAAGTGAGA
GCCATTGTGAGAATCAGCAAGAACATCGCCATCCTCACACCAACTCTGGACTGACCTGG
GGATTGGAGTAGCCACTGTCATCGATGACAGATCCCTGGCCTTCCACATTATCTTCTCC
CTGCTCAATGCATTCCAGGGTTCTCATCCTAGTGTGTTGGAACCACATCCTGGATCCAAAG
GTA

1000 900 800 700 600 500 400 300 200 100

Figure 8

Sequence Name:

GW.S.ctg16790-000000.13.0

Figure 8A

GTGDWSSEGCSTEVRPEGTVCCCDHLTFALLLPTLDQSTVHILTRISQAGCCVSMIFL
AFTIILYAFRLRSRERFKSEDAPKIHVALGGSLFLLNLAFLVNVGSGSKGDAACWARGA
VFHYFLLCAFTWMGLEAFHLYLLAVRVFNTYFGHYFLKLSLVGWGLPALMVGITGSANSY
GLYTIRDRENRTSLELCWFRETTMYALYITVHGYFLITFLFGMVVLALVWKIFTLSRA
TAVKERGKNRKKVLTLGLSSLVGVTVGLAIFTPLGLSTVYIFALFNSLQVDFYILIFY

Figure 8B

GGGACCACTGGAGACTGGTCTCTGAGGGCTGCTCCACGGAGGTCAAGACCTGAGGGGACC
GTGTGCTGCTGTGACCACCTGACCTTTTCGCCCTGCTCCTGAGACCCACCTGGACCAG
TCCACGGTGCATATCCTCACACGCATCTCCAGGCAGGGCTGTGGGGTCTCCATGATCTC
CTGGCCTCACCATTATTCTTATGCCTTCTGAGGCTTCCCGGGAGAGGTTCAAGTCA
GAAGATGCCCAAAGATCCACGTGGCCCTGGGTGGCAGCCTGTTCTCCTGAATCTGGCC
TTCTTGGTCAATGTGGGGAGTGGCTCAAAGGGGTCTGATGCTGCTGCTGGGCCGGGG
GCTGTCTTCACTACTTCTGCTCTGTGCCCTCACCTGGATGGGCTTGAAAGCCTCCAC
CTCTACCTGCTCGCTGTCAAGGTCTTCAACACCTACTTCGGGACTACTTCCTGAAGCTG
AGCCTGGTGGCTGGGCCTGCCCTGATGGTCATCGGCACCTCTGGAGCTATGCTGGTTC
TACGGCCTCTACACCATCCGTGATAGGGAGAACCGCACCTCTGGAGCTATGCTGGTTC
CGTGAAGGGACAACCATGTACGCCCTATATCACCGTCCACGGCTACTTCCTCATCACC
TTCCTCTTGGCATGGTGGCTGGCCCTGGTGGCTGGAGATCTCACCTGTCCCGT
GCTACAGCGGTCAAGGAGCGGGGAGAACCGGAAGAACGGTGTGCTACCCGTGGCCTC
TCGAGCCTGGTGGGTGTGACATGGGGTTGCCATCTCACCCGTGGCCTCTCCACC
GTCTACATCTTGCACCTTCAACTCCTGCAAGTTGATTTACATATTGATCTTCTAT

Figure 9

Sequence Name:

GW.S.ctg12776-000000.172.0

Figure 9A

NHILD TAA IS NWAF I P N K N A S S D L L Q S V N L F A R Q L H I H N N S E N I V N E L F I Q T K G F H I N H N
T S E K S L N F S M S M N N T T E D I L G M V Q I P R Q E L R K L W P N A S Q A I S I A F P T L G A I L R E A H L Q N V
S L P R Q V N G L V L S V V L P E R L Q E I I L T F E K I N K T R N A R A Q C V G W H S K K R R W D E K A C Q M M L D I
R N E V K C R C N Y T S V V M S F S I L M S S K S M T D K V L D Y I T C I G L S V I L S L V L C L I E A T V W S R V
V V T E I S Y M R H V C I V N I A V S L L T A N V W F I I G S H F N I K A Q D Y N M C V A V T F F S H F F Y L S L F F W
M L F K A L L I I Y G I L V I F R R M M K S R M M V I G F A I G Y G C P L I I A V T T V A I T E P E K G Y I R P E A C W
L N W D N T K A L X A F A I P A F V I V A V N L I V V L V V A V N T Q R P S I G S S K S Q D V V I I M R I S K N V A I L
T P L L G L T W G F G I A T L I E G T S L T F H I I F A L L N A F Q F I L L F G T I M D H K V

Figure 9B

A A C C A C A T C C T C G A C A C A G C A G G C A T T C A A A C T G G G C T T C A T T C C C A A C A A A A T G C C
A G C T C G G A T T T G T T G C A G T C A G T G A A T T G T T G C C A G A C A A C T C C A C A T C C A C A A T A A T
T C T G A G A A C A T T G T G A A T G A A C T C T T C A T T C A G A C A A A A G G G T T C A C A T C A A C C A T A A T
A C C T C A G A G A A A A G C C T C A A T T C T C C A T G A G C A T G A A C A A T A C C A C A G A A G G A T A T C T T A
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